

FIG. 1A

1 GGTCTACTAAATATTATTCACATATACATTAATACACAGAAATATCTGCTGTTGGTATTCTGCAATGAATAAGGAGGATAAAGA GTG
 99 AGA GGC AAA AAA GTA TGG ATC AGT TTG CTG TTT GCT ITA GCG ITA ATC TTT ACG ATG GCG TTC GGC AGC ACA TCC
 174 TCT GCC CAG CCG GCA GGG AAA TCA AAC GGG GAA MAG AAA TAT ATT GTC GGG TTT AAA CAG ACA ATG AGC ACG ATG
 249 Ser Ala Ala Lys Lys Lys Asp Val Ile Ser Glu Lys Lys Tyr Ile Val Gly Phe Lys Gln Thr Met Ser Thr Met
 324 Ala Ser Ala Thr Leu Asn Glu Lys Ala Val Lys Glu Lys Glu Lys Lys Phe Lys Tyr Val Asp Ala
 399 His Val Ala GCA CAT CCG TAC CCG CAG TCC GTG CCT TAC GGC GTA TCA CAA ATT AAA GCC CCT GCT CTG CAC TCT CAA
 474 GGC TAC ACT ACT GGA TCA AAT GTT AAA GTA GCG GTT ATC GAC AGC GGT ATC Asp Ser Gly Ile, Asp Ser Ser His Pro Asp Leu Lys Val
 PRE -100 -90 -80 -70 -60 -50 -40 -30 -20 -10 10 20 30 40
 P ⑤ ③ ④
 RBS
 -107 Met
 MAT
 1 1

FIG..1B - 1

FIG. 1B-2

250 Gln
 Val Arg Ser Ser Leu Leu Thr Thr Lys Leu Gly Asp Ser Phe Tyr Tyr Gly Lys Gly Leu Ile Asn
 1149 CAA GTC CGC AGC AGT TTA GAA AAG ACC ACT ACA AAA CTT GGT GAT TCT TTC TAC TAT GGA AAA GGG CTG ATC AAC

270 Val Gln Ala Ala Ala Gln OC
 1224 GTA CAG GCG GCA GCT CAG TAA AACAATAAAACCGCGCTTGGCCCGCGGTTTATTTTCTTCTCGCGCATGTTCAATCGGCTCC
 TERM

1316 ATAAATCGACGGATGGCTCCCTCTGAAAATTTTAACGAGAACCGCGGGTTCACCCCGCTCAGTCCCGTAACGGCCAGTCTCGAAGCTCTCAATCGCGG

1416 CTTCCCGGTTTCCGGTCAGCTCAATGCCGTACGGTGGCGGGGTTTTCTCTGATACCGGGACACGGCATTCGTAATCGGATC

FIG._1B - 3

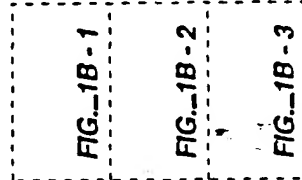


FIG._1B

CONSERVED RESIDUES IN SUBTILISINS FROM
BACILLUS AMYLOLIQUEFACIENS

1	10	20
A Q S V P . G	A P A . H . . .	G
21	30	40
. T G S . V K V A V . D . G	H P	
41	50	60
D L . . . G G A S . V P	Q D	
61	70	80
. N . H G T H V A G T . A A L N N S I	G	
81	90	100
V L G V A P S A . L Y A V K V L G A .	G	
101	110	120
S G . . S . L . . G . E W A . N		
121	130	140
V . N . S L G . P S . S	A . .	
141	150	160
. G V . V V A A . G N . G . . .		
161	170	180
. Y P . . Y	A V G A .	
181	190	200
D . . N . . A S P S . . G . . L D . . .	A	
201	210	220
P G V . . Q S T . P G . . Y	N G T	
221	230	240
S M A . P H V A G A A A L	K . . .	
241	250	260
W . . . Q . R . . L . N T	L G . .	
261	270	
. . Y G . G L . N . . A A . .		

FIG._2

COMPARISON OF SUBTILISIN SEQUENCES FROM:

B. amyloliquefaciens

B. subtilis

B. licheniformis

B. lentus

01	10	20	30
A Q S V P Y G V S Q I K A P A L H S Q G Y T G S N V K V A V I D S G I D S S H P			
A Q S V P Y G I S Q I K A P A L H S Q G Y T G S N V K V A V I D S G I D S S H P			
A Q T V P Y G I P L I K A D K V Q A Q G F K G A N V K V A V L D T G I Q A S H P			
A Q S V P W G I S R V Q A P A A H N R G L T G S G V K V A V L D T G I S T * H P			
41	50	60	70
D L K V A G G A S M V P P S E T N P P Q D D N N S H G T H V A G T V A A L N N S I G			
D L N V R G G A S P V P S E T N P Y Q D G S S H G T H V A G T I A A L N N S I G			
D L N V V G G A S P V A G E A Y N * T D G N G H G T H V A G T V A A L D N T T G			
D L N I R G G A S P V P G E * P S T Q D D G N G H G T H V A G T I A A L N N S I G			
81	90	100	110
V L G V A P S A S L Y A V K V L G A D G S G Q Y S W I I N G I E W A I A N N M D			
V L G V S P S A S L Y A V K V L D S T G S G Q Y S W I I N G I E W A I S N N M D			
V L G V A P S V S L Y A V K V L N S S G S G S Y S G I V S G I E W A T T N G M D			
V L G V A P S A E L Y A V K V L G A S G S G S V S S I A Q Q G L E W A G N N G M H			
121	130	140	150
V I N M S L G G P S G S A A L K A A V D K A V A S G V V V V A A A G N E G T S G			
V I N M S L G G P T G S T A L K T V V D K A V S S G I V V V A A A G N E G S S G			
V I N M S L G G A S G S T A M K Q A V D N A Y A R G V V V V A A A G N S G N S G			
V A N L S L G S P S A T L E Q A V N S A T S R G V L V V A A S G N S G A G S			

FIG._3A

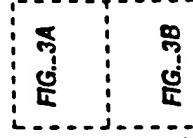
161 SSSTVGYPGKYPSSVIAVGAVDSSNQRASSFSSVGPPELDDVMA
 170 STSTVGYPPAKYPSTIAVGAVDSSNQRASSFSSAGSELDVMA
 STNTIGYPPAKYDSSVIAVGAVDSSNSNRASFFSSVGALEEVMA
 180 ***ISYPARYANAMAVGATDQNNNRASFSQYGGAGLDIVA

201 PGVSIQSTLPGNKKYGAYNNGTSMASPHVAGAAALILSKHHPN
 210 PGVSIQSTLPGGTTYGAYNNGTSMATPHVAGAAALILSKHPT
 PGAGVYSTYPTNTYATLNGTSMASPHVAGAAALILSKHHPN
 220 PGVNVQSSYYPGSTYASLNGTSMATPHVAGAAALVKQKNPS

241 WTNNTQVRSLSLENTTTKLGGDSFYYGKGLINVQAAAO
 250 WTNAAQVRRDRLESTATTYLGNSFFYYGKGLINVQAAAO
 WLSAQVRRNRLSSTATTYLGSSFFYYGKGLINVEAAAO
 260 WSNVQIRNNHLKNTATSLGSTNLYGSGLVNAEAAATR

FIG._3B

FIG._3



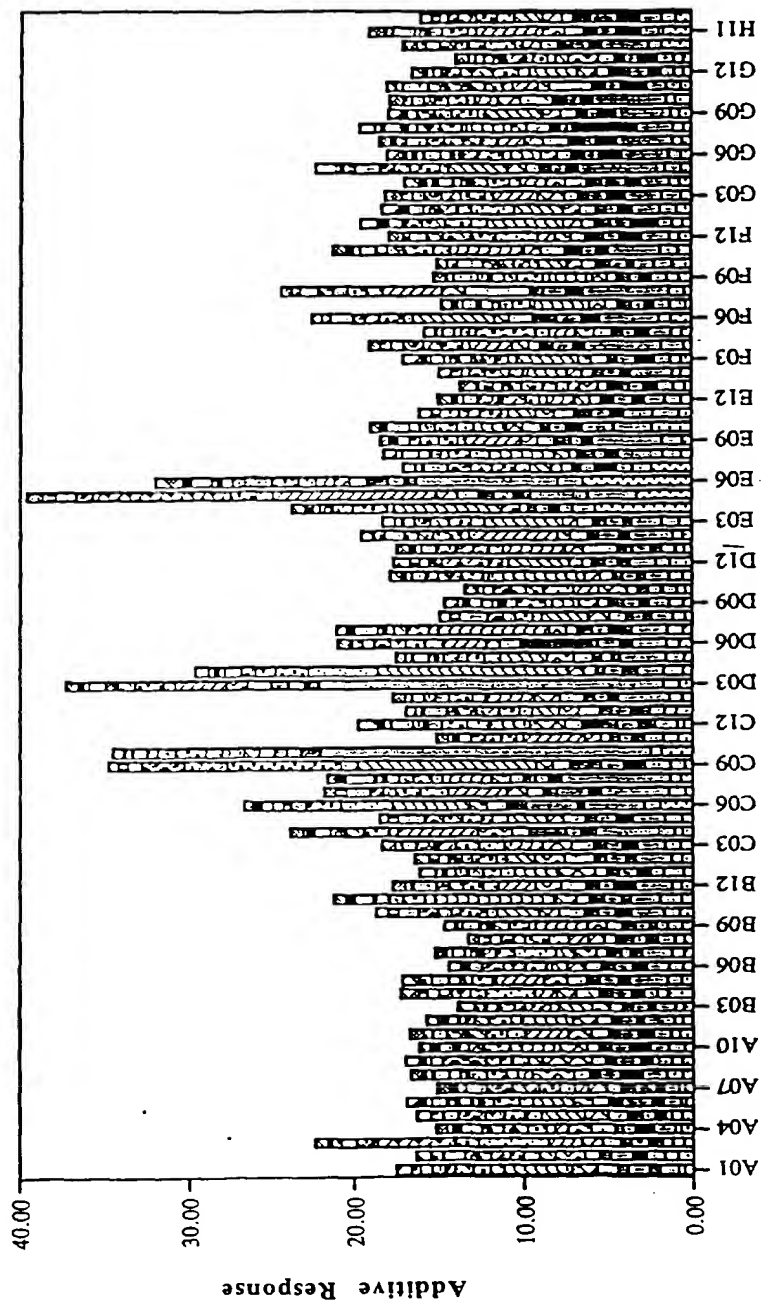


FIG. 4

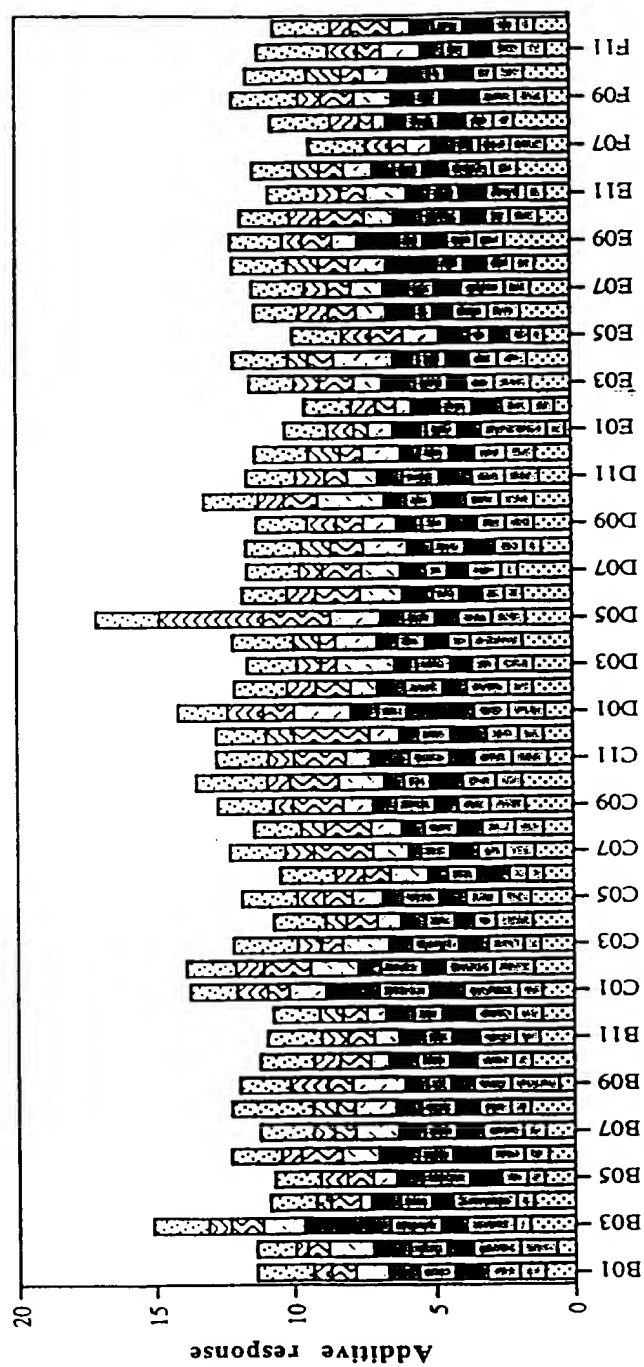


FIG. 5

7435

Page 33

1	A12	IKDFHVYFRESRDAG	49	E12	SATSRGVLVVAASGN
2	A11	LEQAVNSATSRGVLV	50	E11	SRGVLVVAASGNSGA
3	A10	AQSVPWGISRVQAPA	51	E10	VLVVAASGNSGAGSI
4	A9	VPWGISRVQAPAAHN	52	E9	VAASGNSGAGSISYP
5	A8	GISRVQAPAAHNRGL	53	E8	SGNSGAGSISYPARY
6	A7	RVQAPAAHNRGLTGS	54	E7	SGAGSISYPARYANA
7	A6	APAAHNRGLTGSGVK	55	E6	GSISYPARYANAMAV
8	A5	AHNRGLTGSGVKVAV	56	E5	SYPARYANAMAVGAT
9	A4	RGLTGSGVKVAVLDT	57	E4	ARYANAMAVGATDQN
10	A3	TGSGVKVAVLDTGIS	58	E3	ANAMAVGATDQNNNR
11	A2	GVKVAVLDTGISTHP	59	E2	MAVGATDQNNNRASF
12	A1	VAVLDTGISTHPDLN	60	E1	GATDQNNNRASFQY
13	B12	LDTGISTHPDLNIRG	61	F12	DQNNNRASFQYGAG
14	B11	GISTHPDLNIRGGAS	62	F11	NNRASFQYGAGLDI
15	B10	THPDLNIRGGASFVP	63	F10	ASFSQYGAGLDIVAP
16	B9	DLNIRGGASFVPGEP	64	F9	SQYGAGLDIVAPGVN
17	B8	IRGGASFVPGEPSTQ	65	F8	GAGLDIVAPGVNVQS
18	B7	GASFVPGEPSTQDGN	66	F7	LDIVAPGVNVQSTYP
19	B6	FVPGEPSTQDGNHGH	67	F6	VAPGVNVQSTYPGST
20	B5	GEPSTQDGNHGHGTHV	68	F5	GVNVQSTYPGSTYAS
21	B4	STQDGNHGHGTHVAGT	69	F4	VQSTYPGSTYASLNG
22	B3	DGNHGHGTHVAGTIAA	70	F3	TYPGSTYASLNGTSM
23	B2	GHGTHVAGTIAALNN	71	F2	GSTYASLNGTSMATP
24	B1	THVAGTIAALNNSIG	72	F1	YASLNGTSMATPHVA
25	C12	AGTIAALNNSIGVLG	73	G12	LNGTSMATPHVAGAA
26	C11	IAALNNSIGVLGVAP	74	G11	TSMATPHVAGAAALV
27	C10	LNNSIGVLGVAPSAE	75	G10	ATPHVAGAAALVKQK
28	C9	SIGVLGVAPSAELYA	76	G9	HVAGAAALVKQKNPS
29	C8	VLGVAPSAELYAVKV	77	G8	GAAALVKQKNPSWSN
30	C7	VAPSAELYAVKVLGA	78	G7	ALVKQKNPSWSNVQI
31	C6	SAELYAVKVLGASGS	79	G6	KQKNPSWSNVQIRNH
32	C5	LYAVKVLGASGSGSV	80	G5	NPSWSNVQIRNHLKN
33	C4	VKVLGASGSGSVSSI	81	G4	WSNVQIRNHLKNTAT
34	C3	LGASGSGSVSSIAQG	82	G3	VQIRNHLKNTATSLG
35	C2	SGSGSVSSIAQGLEW	83	G2	RNHLKNTATSLGSTN
36	C1	GSVSSIAQGLEWAGN	84	G1	LKNTATSLGSTNLYG
37	D12	SSIAQGLEWAGNNGM	85	H12	TATSLGSTNLYGSGL
38	D11	AQGLEWAGNNGMHVA	86	H11	SLGSTNLYGSGLVNA
39	D10	LEWAGNNGMHVANLS	87	H10	STNLYGSGLVNAEAA
40	D9	AGNNGMHVANLSLGS	88	H9	NLYGSGLVNAEAATR
41	D8	NGMHVANLSLGSPSP			
42	D7	HVANLSLGSPSPSAT			
43	D6	NLSLGSPSPSATLEQ			
44	D5	LGSPSPSATLEQAVN			
45	D4	PSPSATLEQAVNSAT			
46	D3	SATLEQAVNSATSRG			
47	D2	LEQAVNSATSRGVLV			
48	D1	AVNSATSRGVLVVA			

FIG. 6A

11 4 35

1	A12	IKDFHVFYFRESRDAG	49	E12	KKIDVLNLSIGGPDF
2	A11	DAELHI FRVFTNNQV	50	E11	DVLNLSIGGPDFMDH
3	A10	PLRRASLSLGSGFWH	51	E10	NLSIGGPDFMDHPFV
4	A9	RASLSLGSGFWHATG	52	E9	IGGPDFMDHPFVDKV
5	A8	LSLGSGFWHATGRHS	53	E8	PDFMDHPFVDKVVWEL
6	A7	GSGFWHATGRHSSRR	54	E7	MDHPFVDKVVWELTAN
7	A6	FWHATGRHSSRLLR	55	E6	PFVDKVVWELTANNVI
8	A5	ATGRHSSRLLRAIP	56	E5	DKVVWELTANNVIMVS
9	A4	RHSSRLLRAIPRQV	57	E4	WELTANNVIMVSAIG
10	A3	SRLLRAIPRQVAQT	58	E3	TANNVIMVSAIGNDG
11	A2	LLRAIPRQVAQTLQA	59	E2	NVIMVSAIGNDGPLY
12	A1	AIPRQVAQTLQADVL	60	E1	MVSAIGNDGPLYGTJ
13	B12	RQVAQTLQADVLWQM	61	F12	AIGNDGPLYGTLNPN
14	B11	AQTLQADVLWQMGYT	62	F11	NDGPLYGTLNPNADQ
15	B10	LQADVLWQMGYTGAN	63	F10	PLYGTLNPNADQMDV
16	B9	DVLWQMGYTGANVRV	64	F9	GTLNPNADQMDVIGV
17	B8	WQMGYTGANVRVAVF	65	F8	NNPADQMDVIGVGGI
18	B7	GYTGANVRVAVFDTG	66	F7	ADQMDVIGVGGIDFE
19	B6	GANVRVAVFDTGLSE	67	F6	MDVIGVGGIDFEDNI
20	B5	VRVAVFDTGLSEKHP	68	F5	IGVGGIDFEDNIARF
21	B4	AVFDTGLSEKHPHFK	69	F4	GGIDFEDNIARFSSR
22	B3	DTGLSEKHPHFKNVK	70	F3	DFEDNIARFSSRGMT
23	B2	LSEKHPHFKNVKERT	71	F2	DNIARFSSRGMTTWE
24	B1	KHPHFKNVKERTNWT	72	F1	ARFSSRGMTTWELPG
25	C12	HFKNVKERTNWTNER	73	G12	SSRGMTTWELPGGYG
26	C11	NVKERTNWTNERTLD	74	G11	GMTTWELPGGYGRMK
27	C10	ERTNWTNERTLDGGL	75	G10	TWELPGGYGRMKPDI
28	C9	NWTNERTLDGGLGHG	76	G9	LPGGYGRMKPDIVTY
29	C8	NERTLDGGLGHGTFV	77	G8	GYGRMKPDIVTYGAG
30	C7	TLDDGGLGHGTFVAGV	78	G7	RMKPDIVTYGAGVRG
31	C6	DGLGHGTFVAGVIAS	79	G6	PDIVTYGAGVRGSGV
32	C5	GHGTFVAGVIASMRE	80	G5	VTYGAGVRGSGVKGG
33	C4	TFVAGVIASMRECQG	81	G4	GAGVRGSGVKGGCRA
34	C3	AGVIASMRECQGFAP	82	G3	VRGSGVKGGCRALSG
35	C2	IASMRECQGFAPDAE	83	G2	SGVKGGCRALSGTSV
36	C1	MRECQGFAPDAELHI	84	G1	KGGCRALSGTSVASP
37	D12	CQGFAPDAELHI FRV	85	H12	CRALSGTSVASPVVA
38	D11	FAPDAELHI FRVFTN	86	H11	LSGTSVASPVVAGAV
39	D10	DAELHI FRVFTNNQV	87	H10	TSVASPVVAGAVTLL
40	D9	LHI FRVFTNNQVSYT	88	H9	ASPVVAGAVTLLVST
41	D8	FRVFTNNQVSYTSWF	89	H8	VVAGAVTLLVSTVQK
42	D7	FTNNQVSYTSWFLDA	90	H7	GAVTLLVSTVQKREL
43	D6	NQVSYTSWFLDAFNY	91	H6	TLLVSTVQKRELVNP
44	D5	SYTSWFLDAFNYAIL	92	H5	VSTVQKRELVNPASM
45	D4	SWFLDAFNYAILKKI	93	H4	VQKRELVNPASMKQA
46	D3	LDAFNYAILKKIDVL	94	H3	RELVNPASMKQALIA
47	D2	FNYAILKKIDVLNLS	95	H2	VNPASMKQALIASAR
48	D1	AILKKIDVLNLSIGG	96	H1	ASMKQALIASARRLP

FIG. 6B

97	I12	IKDFHVYFRESRDAG
98	I11	DAELHIFRVFTNNQV
99	I10	KQALIASARRLPGVN
100	I9	LIASARRLPGVNMFE
101	I8	SARRLPGVNMFEQGH
102	I7	RLPGVNMFEQGHGKL
103	I6	GVNMFEQGHGKLDLL
104	I5	MFEQGHGKLDLLRAY
105	I4	QGHGKLDLLRAYQIL
106	I3	GKLDLLRAYQILNSY
107	I2	DLLRAYQILNSYKPQ
108	I1	RAYQILNSYKPQASL
109	J12	QILNSYKPQASLSPS
110	J11	NSYKPQASLSPSYID
111	J10	KPQASLSPSYIDLTE
112	J9	ASLSPSYIDLTECPY
113	J8	SPSYIDLTECPYMWP
114	J7	YIDLTECPYMWPYCS
115	J6	LTECPYMWPYCSQPI
116	J5	CPYMWPYCSQPIYYG

FIG. 6C

MKLVNIWLLLLLVLLCGKKHLGDRLEKKSFEKAPCPGCSHLTLKVEFSSTVVEYEYIVAFNGYFT
AKARNSFISSALKSSEVDNWRIIPRNNPSSDYPSDFEVIQIKEKQKAGLLTLEDHPNIKRVTQOR
KVFRSLKYAESDPTVPCNETRWSQKWQSSRPLRRASLSLGSGFWHATGRHSSRLLRAIPRQVAQ
TLQADVLWQMGYTGANVRVAVFDTGLSEKHPHFKNVKERTNWTNERTLDDGLGHGTFVAGVIASM
RECQGFAPDAELHIFRVFTNNQVSYTSWFLDAFNAYAILKKIDVLNLSIGGPDFMDHPFVDKVVWEL
TANNVIMVSAIGNDGPLYGTLNNPADQMDVIGVGGIDFEDNIARFSSRGMTTWELPGGYGRMKPD
IVTYGAGVRGSGVKGGCRALSGTSVASPVVAGAVTLLVSTVQKRELVPASMKQALIASARRLPG
VNMFEQGHGKLDLLRAYQILNSYKPQASLSPSYIDLTECPYMWPYCSQPIYYGGMPTVVNVITILN
GMGVTGRIVDKPDWQPYLPQNGDNIEVAFSYSSVLWPWSGYLAISISVTKKAASWEGIAQGHVMI
TVASPAETESKNGAEQTSTVKLPIKVKIIPTPPRSKRVLWDQYHNLRYPPGYFPRDNLRMKNDPL
DWNGDHIIHTNFRDQMYQHLRSMGYFVEVLGAPFTCFDASQYGTLLMVDSEEEYFPEEIAKLRRDVD
NGLSLVIFSDWYNTSVMRKVKFYDENTRQWWMPDTGGANIPALNELLSVWNMGFSDGLYEGETL
ANHDMYASGCSIAKFPEDGVVITQTFKDQGLEVLKQETAVVENVPILGLYQIPAEGGGRIVLYG
DSNCLDDSHRQKDCFWLLDALLQYTSYGVTPPSLSHSGNRQRPPSGAGSVTPERMEGNHLHRYSK
VLEAHLGDPKPRPLPACPRLSWAKPQPLNETAPSNLWKHQKLLSIDLDKVVLNFRSNRPQVRPL
SPGESGAWDIPGGIMPGRYNQEVGQTI PVFAFLGAMVVLAFVQINKAKSRPKRRKPRVKRPQL
MQQVHPPKTPSV

FIG. 7

14 4 35

	10	20	30	40	50	
BPN'	AQSVPYGV SQ- IKAPALHSQGYTG SNVKVAVIDSGIDSSHPDLK-VAGGA					48
SAVINASE	AQSVPWGI SR-VQAPAAHNRGLTGSGVKVAVLDTGI-STHPDLN-IRGGA					47
S2HSBT	-RAIPRQVAQTLQADV LWQMGYTGANVRVAVFDTGLSEKHPHFKNVKERT					49
	60	70	80	90	100	
BPN'	SMVPSETNPFQDNNSHGTHVAGTVAAALNNSIGVLGVAPSASLYAVKVLGA					98
SAVINASE	SFVPGEPST-QDGNHGHGTHVAGTIAALNNSIGVLGVAPSAELYAVKVLGA					96
S2HSBT	NW--TNERTLDDGLGHGTFVAGVIASMRECQGF---APDAELHIFRVFTN					94
	110	120	130	140	150	
BPN'	DGSGQYSWIINGIEWAIANNMDVINMSLGGPS-GSAALKA AVDKAVASGV					147
SAVINASE	SGSGSVSSIAQGLEWAGNNGMHVANLSLGSPS-PSATLEQAVNSATSRGV					145
S2HSBT	NQVSYTSWFLDAFN YAILKKIDVLNLSIGGPDFMDHPFVDK VWELTANNV					144
	160	170	180	190	200	
BPN'	VVVAAAGNEGTS GSSSTVGYPGKYPSVIAVGAVDSSNQ RASFSSVGP EL-					197
SAVINASE	LVVAASGNSGA---GSISYPARYANAMAVGATDQNNNRASF SQYGAGL-					191
S2HSBT	IMVSAIGNDGP--LYGTLNNPADQMDVIGVGGIDFEDNIARFSSRGMTTW					192
	210	220	230	240	250	
BPN'	-----DVMA PGVSIQSTLPGNKYGAYNGTSMASPHVAGAAALIL					235
SAVINASE	-----DIVAPGVNVQSTYPGSTYASLNGTSMATPHVAGAAALVK					229
S2HSBT	ELPGGYGRMKPDIVTYGAGVRGSGVKGGCRALSGT SVASPVVAGAVTLLV					242
	260	270	280	290		
BPN'	SKHPNWTNTQ---VRSSLENTTTKLGD SFYYGKGLINVQAAAQ					275
SAVINASE	QKNPSWSNVQ---IRNHLKNTATSLGSTNLYGSGLVNAEAATR					269
S2HSBT	STVQKREL VNPASMKQALIASARRLPGVNMFEQG-----HGKL					280

FIG. 8

15 4 35

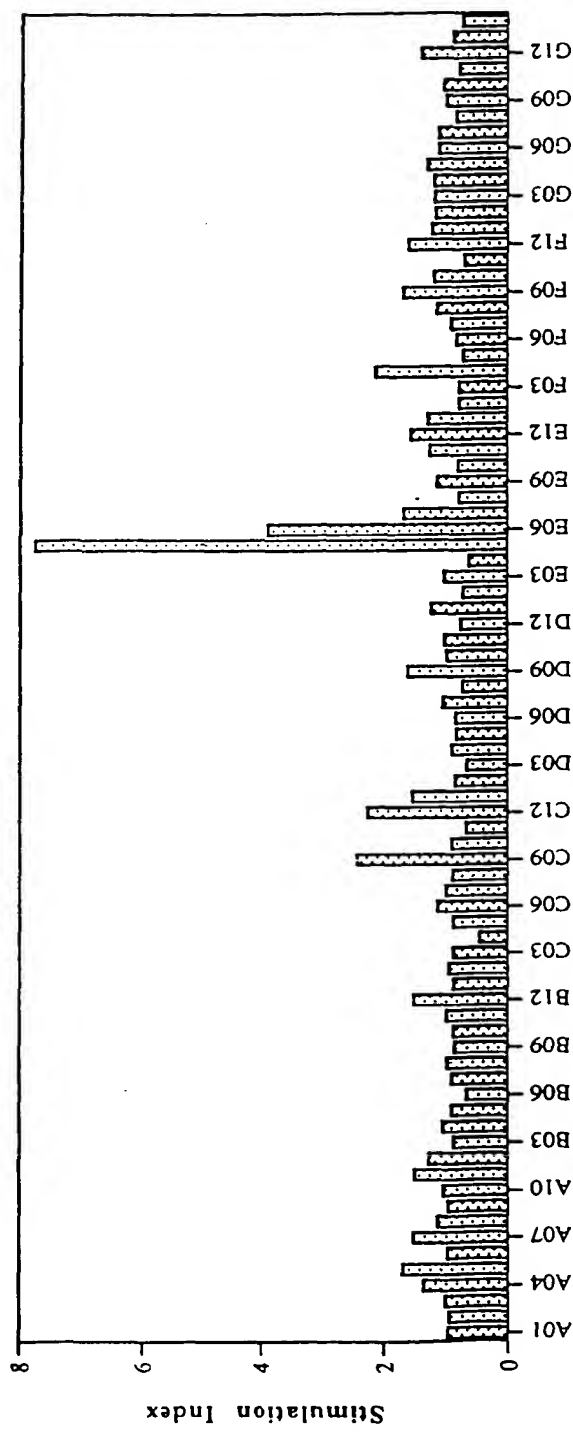


FIG. 9

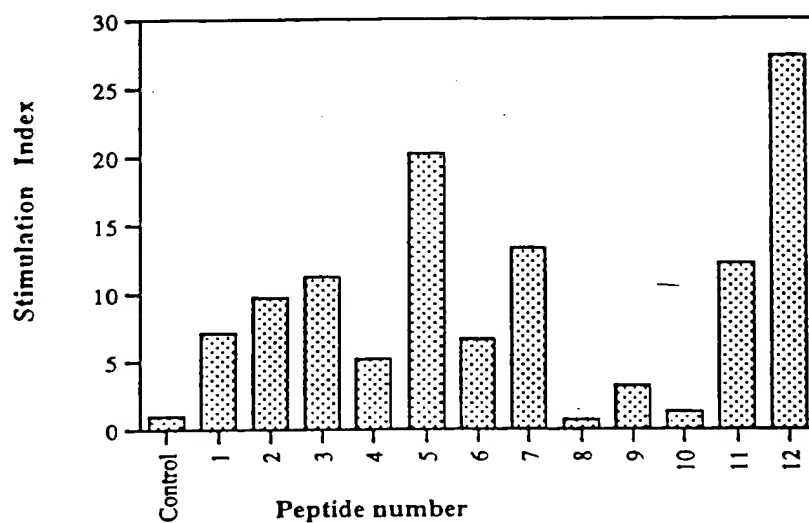
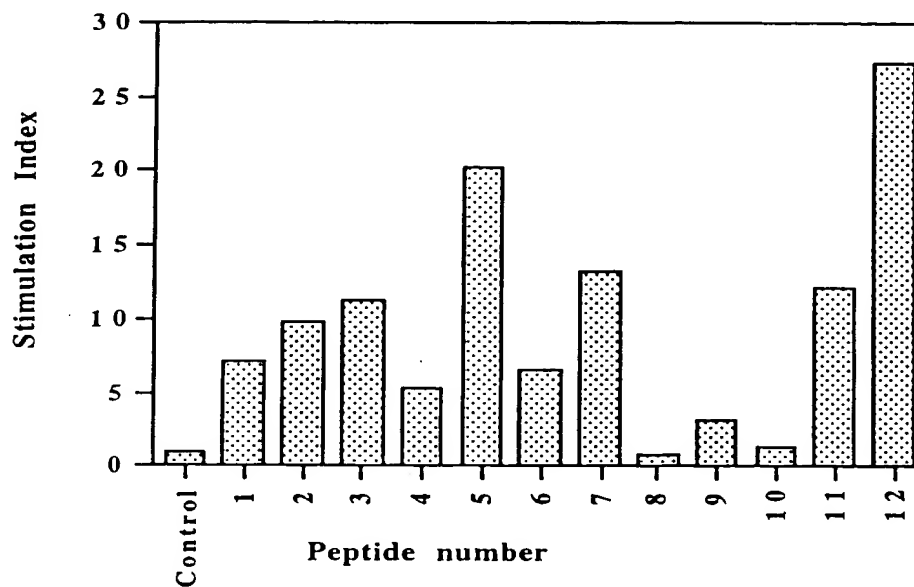


FIG. 10



Peptide number	Sequence
1 (unmodified sequence)	GSISYPARYANAMAV
2	ASISYPARYANAMAV
3	GAISYPARYANAMAV
4	GSASYPARYANAMAV
5	GSIAYPARYANAMAV
6	GSISAPARYANAMAV
7	GSISYAARYANAMAV
8	GSISYPAAAYANAMAV
9	GSISYPARAANAMAV
10	GSISYPARYAAAMAV
11	GSISYPARYANAAAV
12	GSISYPARYANAMAA

FIG. 11

18 of 35

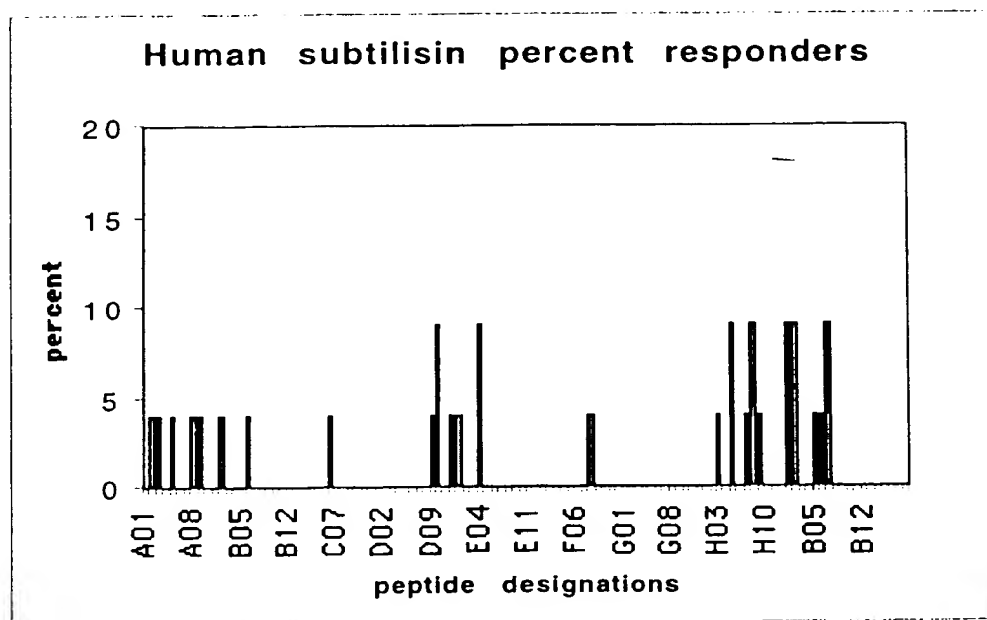


FIG. 12

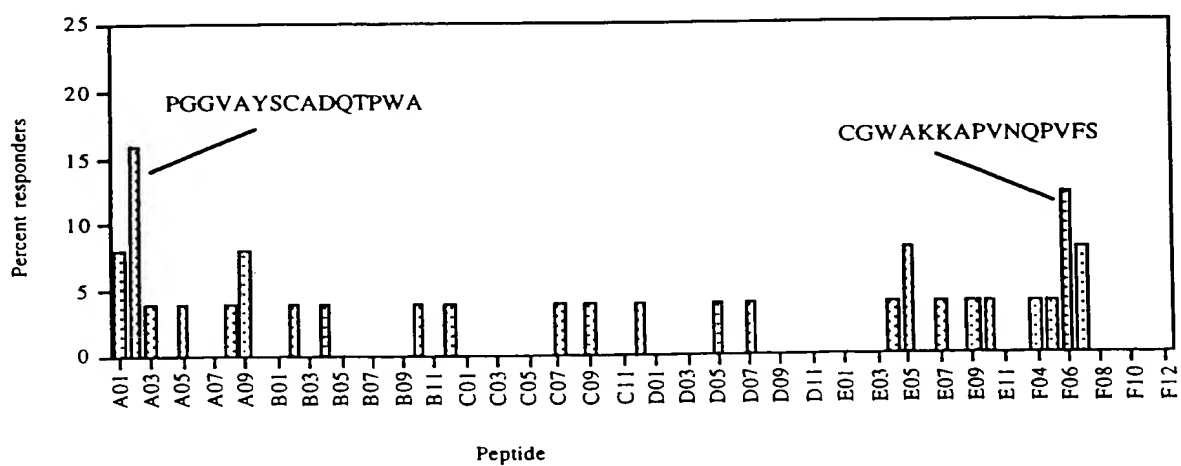


FIG. 13A

1	2	3	4	5
1234567890	1234567890	1234567890	1234567890	1234567890
MRSSPLLPSA	VVAALPVLAL	AADGRSTRYW	DCCKPSCGWA	KKAPVNQPVF
SCNANFQRIT	DFDAKSGCEP	GGVAYSCADO	TPWAVNDDFA	LGFAATSIAG
SNEAGWCCAC	YELTFTSGPV	AGKKMVVQST	STGGDLGSNH	FDLNIPGGGV
GIFDGCTPQF	GGLPGQRYGG	ISSRNECDRF	PDALKPGCYW	RFDWFKNADN
PSFSFRQVQC	PAELVARTGC	RRNDDGNFPA	VQIPSSSTSS	PVNQPTSTST
TSTSTTSSPP	VQPTTPSGCT	AERWAQ		

FIG. 13B

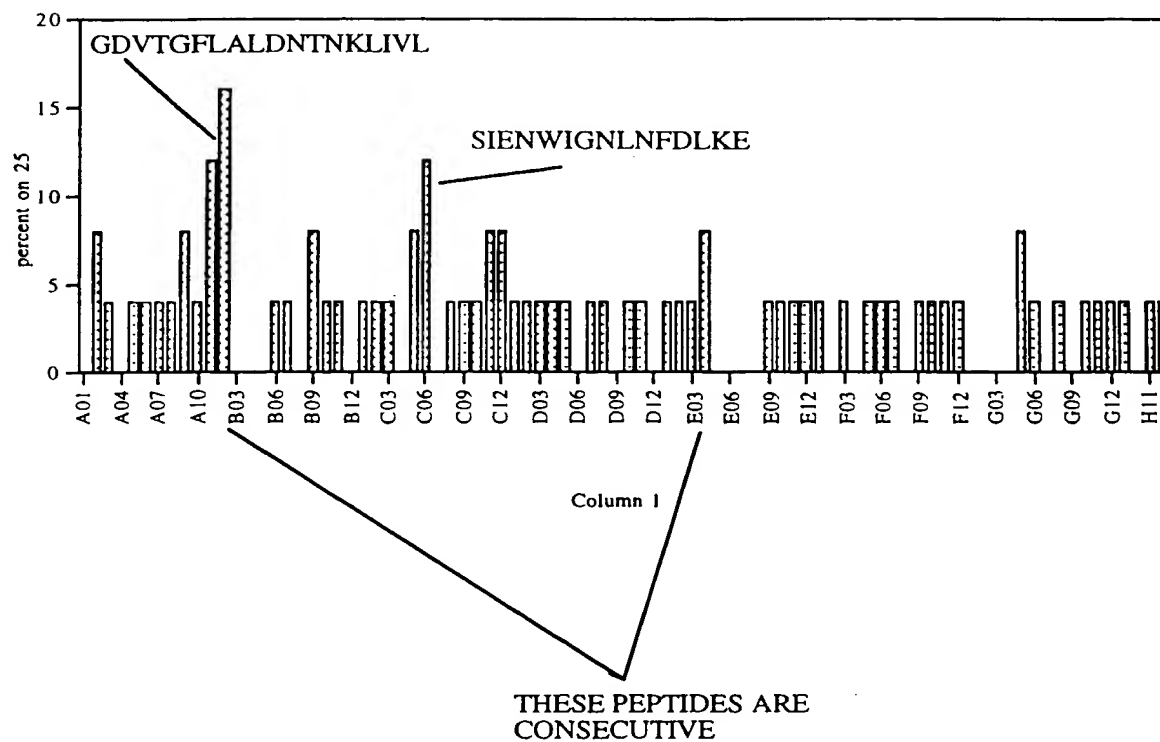


FIG. 14A

1 mrsslvlfv sawtalaspi rrevsqdlfn qfnlfaqysa aaȳcgknnda
51 pagtnitctg nacpevekad atflysfeds gvqdv~~t~~qfla ldntnklivl
101 sfrgsrsien wignlnfdlk eindicgcr ghdgftsswr svadtlrqkv
151 edavrehpdy rvvftghslg galatvagad lrgngydidv fsygaprvgn
201 rafaefltvq tggtyrith tndivprlpp refgyshssp eywiksgtlv
251 pvtrndivki egidatggnn qpnipdipah lwyfgligtc 1

FIG. 14B

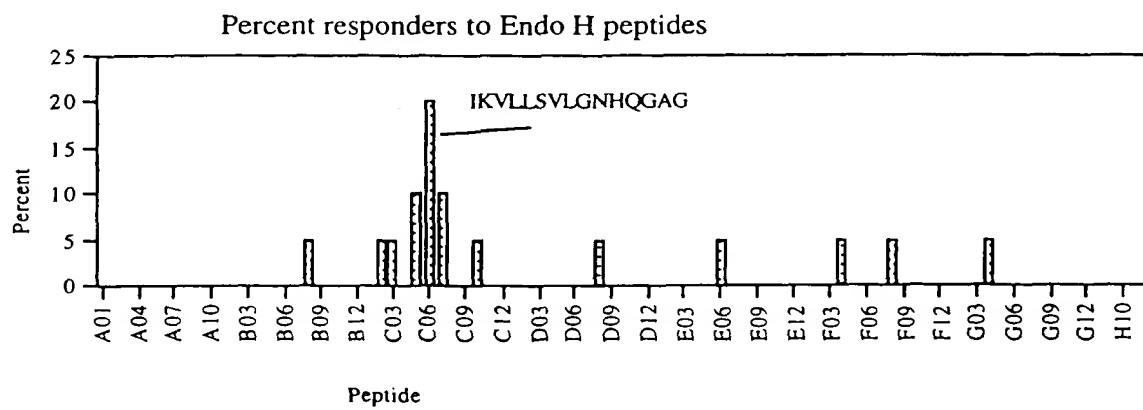


FIG. 15A

1 mftpvrrrvr taalalsaaa alvlgstaas gasatpspap apapapvkqg
51 ptsvayvevn nnsmlnvgy tladgggnaf dvavifaani nydtgktay
101 lhfnevnqrv ldnvtqirp lqqggikvll svlgnhqqaq fanfpsqqa
151 safakqlsda vakygldgvd fddeyaeygn ngtaqpndss fvhlvtalra
201 nmpdkiiisly nigpaasrls yggvdvskf dyawnpyygt wqvpqialpk
251 aqlspaavei grtsrstvad larrtvdegy gvyltynldg gdrtadv saf
301 trelygseav rtp

FIG. 15B

25 y 35

Percent of responders

BPN compiled for 22 individuals.

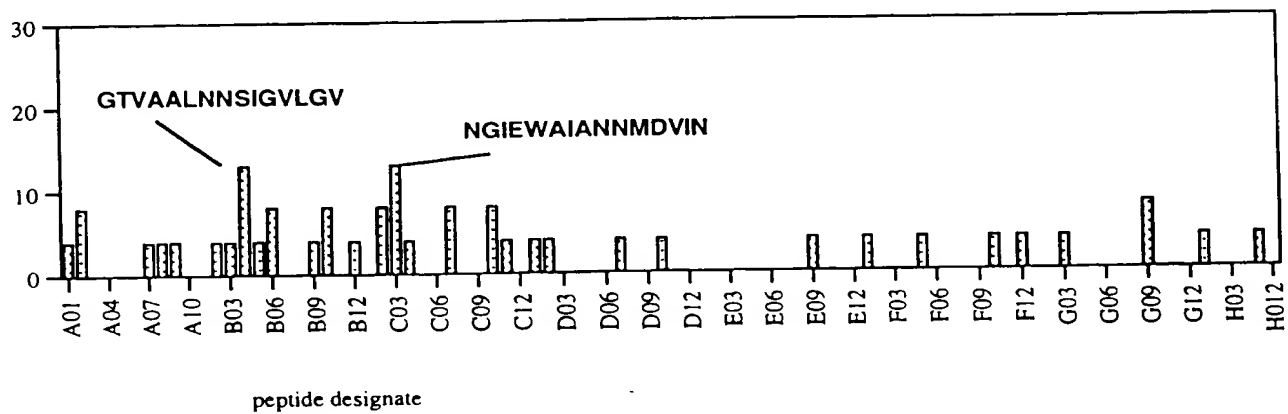


FIG. 16

26 of 33

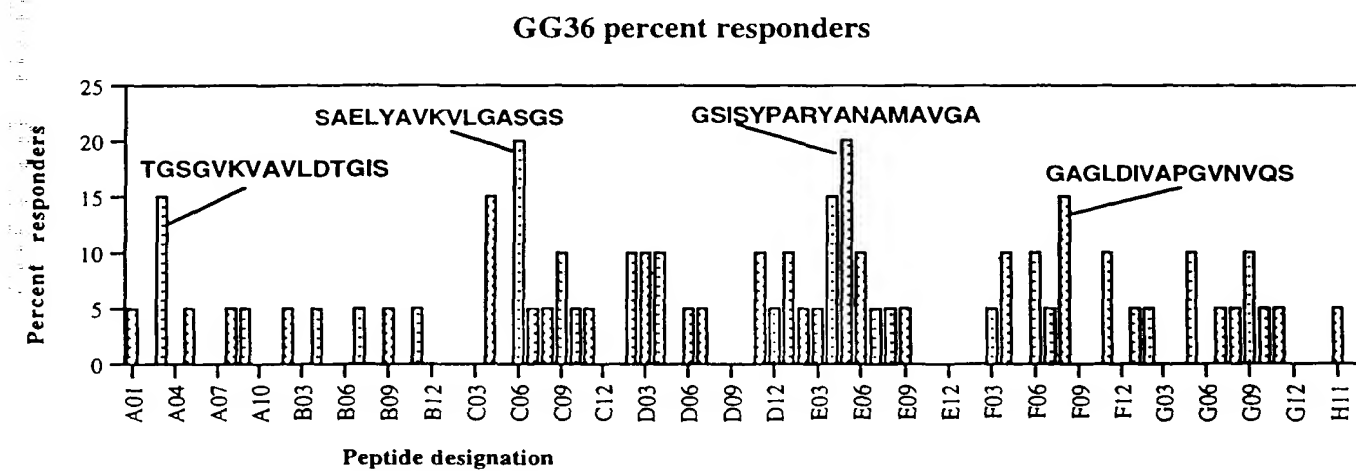


FIG. 17

Hybrid enzyme sequence (GG36-BPN)

GG36

AQSVPWGISRVQAPAAHNRGLTGSGVKVAVLDTGISTHPDLNIRGGASFVPGEPTQDGNGH

BPN

GTHVAGTIAALNNSIGVLGVAPSAELYAVKVLGASGSGSVSSIAQGLEWAGNNGMHVINMSLGGG

Δ

GSAALKAAVDKAVASGVVVVAAAAGNEGTSGSSSTVGYPGKYPSVIAVGAVDSSNQRASFSSVGP

ELDVMAPGVSIQSTLPGNKYGAYNGTSMASPHVAGAAALILSKHPNWTNTQVRSSLENTTTKLGD

SFYY GKGLINVQAAAQ

FIG. 18

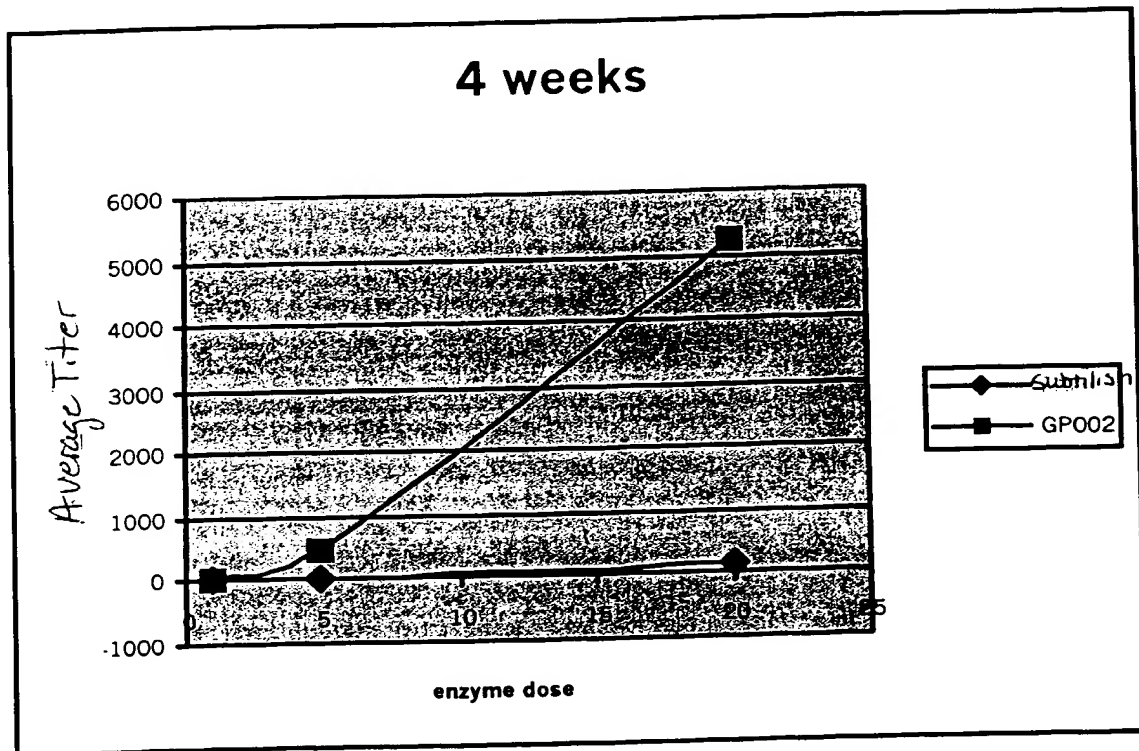


FIGURE 19A

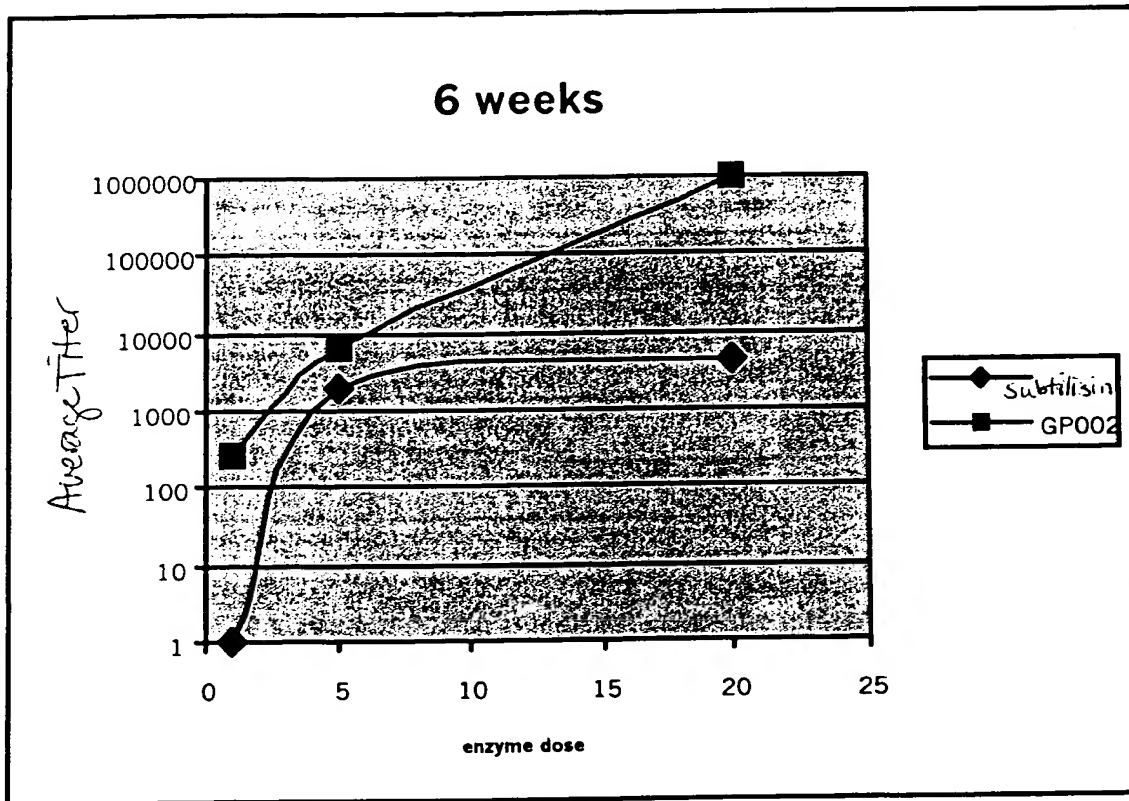


FIGURE 19B

30 of 35

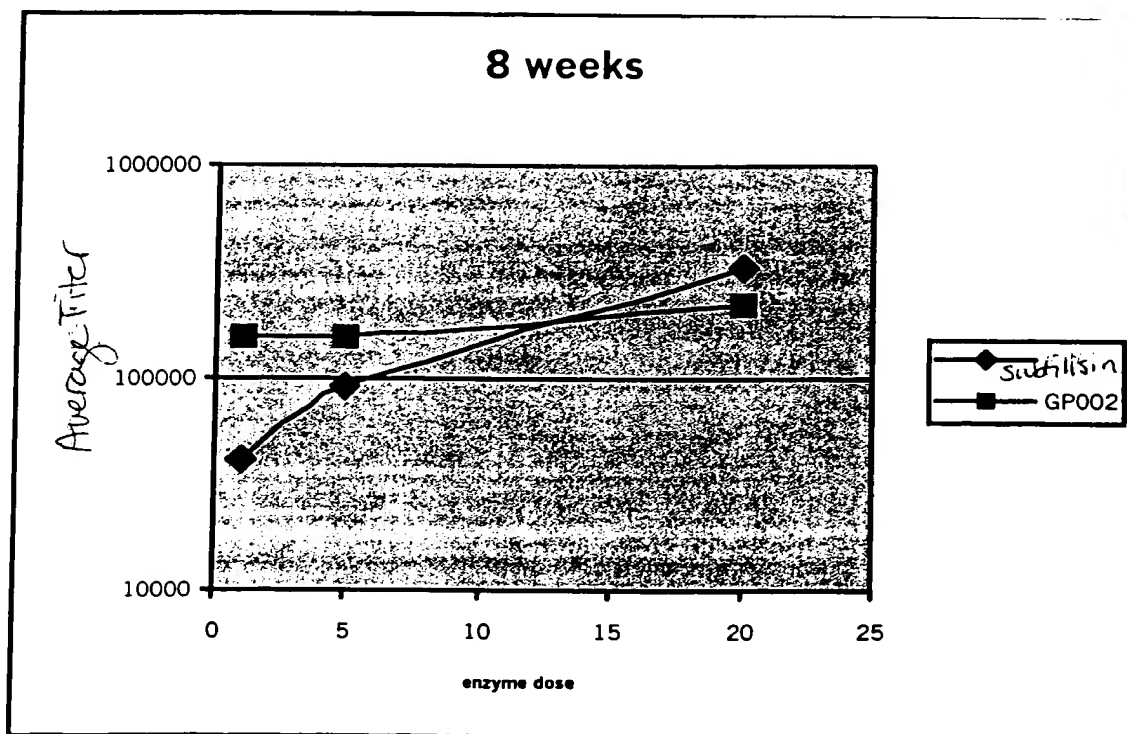


FIGURE 19C

31 2/ 35

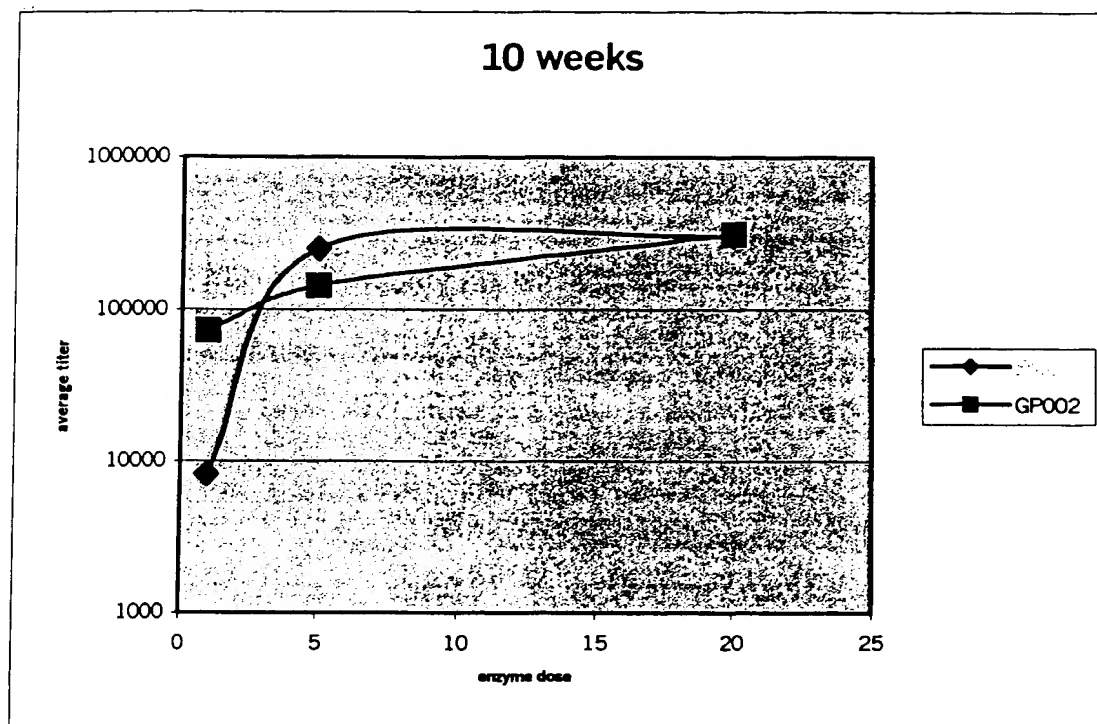


FIGURE 19D

82 of 35

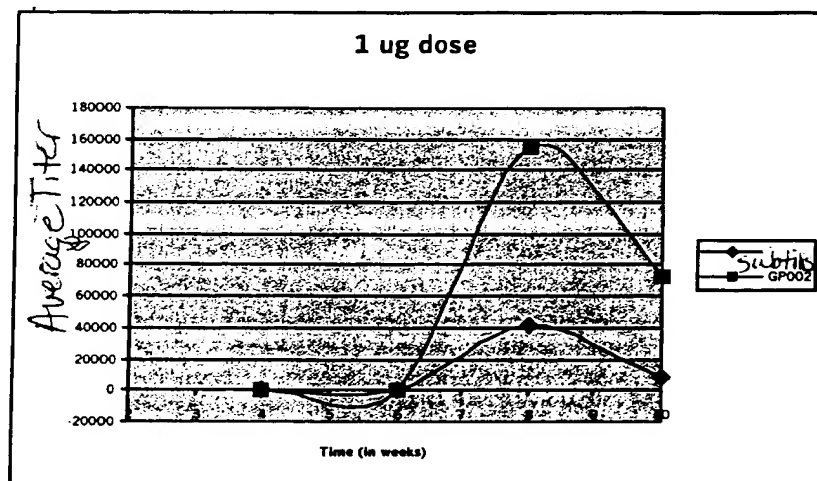


FIGURE 20A

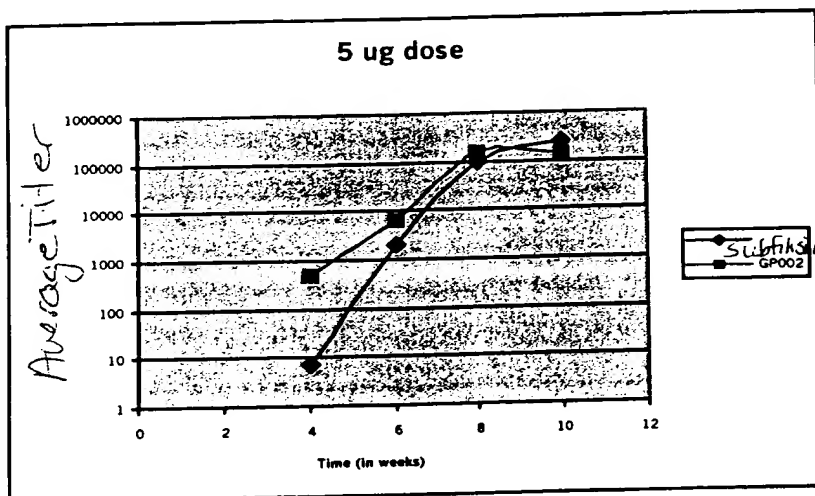


FIGURE 20B

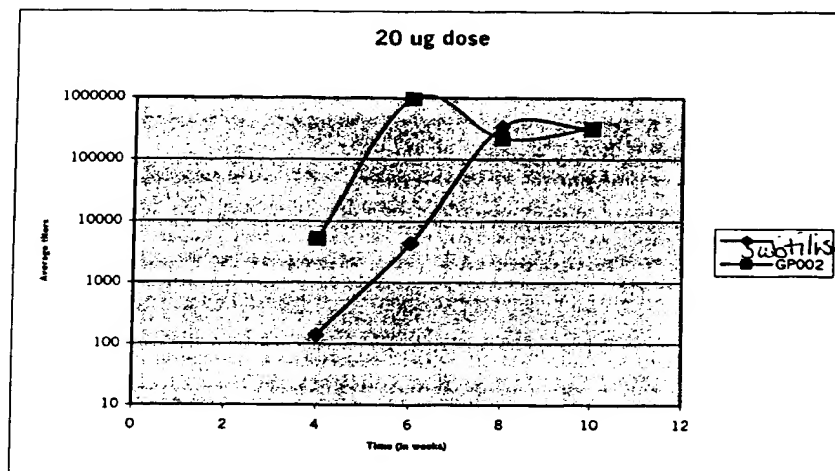


FIGURE 20C

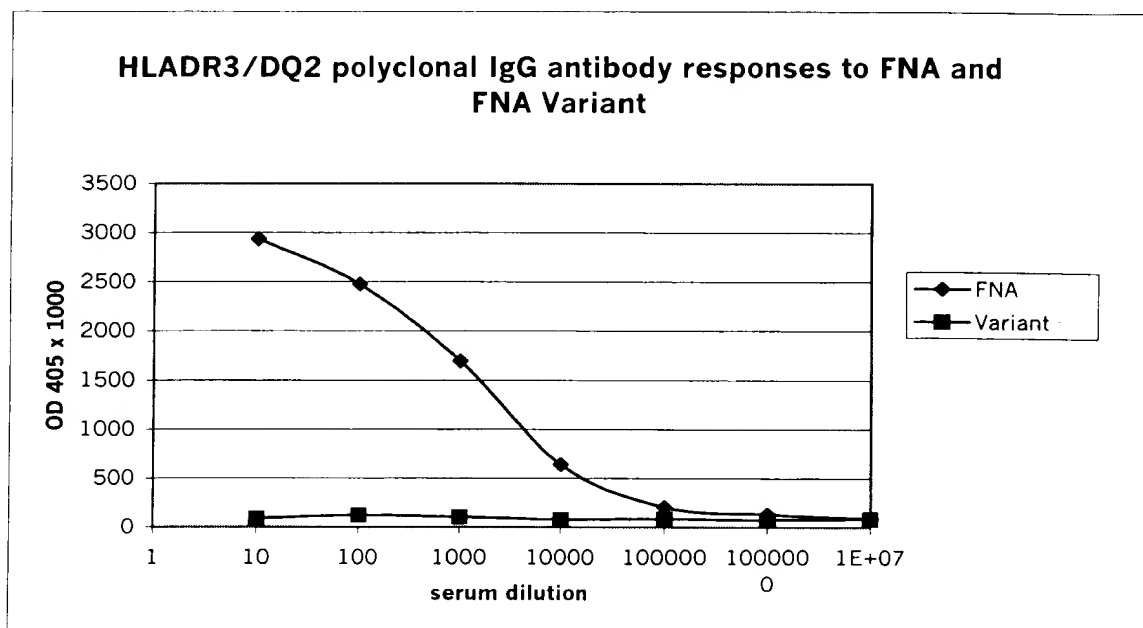


FIGURE 21